SP22	1	MASKRALVILAKGAEEMETVIPVDIMRRAGIK <u>VTVAGLAGKDPVQCSR</u> DV	50
DJ-1	1	MASKRALVILAKGAEEMETVIPVDVMRRAGIK <u>VTVAGLAGKDPVQCSR</u> DV	50
		Peptide 1	
SP22	51	VICPDTSLEEAKTQGPYDVVVLPGGNLGAQNLSESALVK <u>EILK</u> EQENRKG	100
DJ-1	51	${\tt VICPDASLEDAKKEGPYDVVVLPGGNLGAQNLSESAAVK} \underline{{\tt EILK}} {\tt EQENRKG}$	100
		Peptide 2	
		- -	
SP22	101	LIAAICAGPTALLAHEVGFGCKV <u>TSHPLAK</u> DKMMNGSHYSYSESRVEKD	149
DJ-1	101	LIAAICAGPTALLAHEIGCGSKV <u>TTHPLAK</u> DKMMNGGHYTYSENRVEK <u>D</u>	149
		Peptide 3	
SP22	150	GLILTSRGPGTSFEFALAIVEALSGKDMANQVKAPLVLKD 189	
DJ-1	150	GLILTSRGPGTSFEFALAIVEALNGKEVAAQVKAPLVLKD 189	
		Peptide 4	

FIGURE 2

1	A	gctgtgcagagccgtctggcagggttgacctcctaaagggatattccatctttattaatcattag	65
66	A	tagtgtggtcagagacttagcaccattggtctcccccaacctggtccagacatttcagcagttta	130
131	A B	$toggaacagcaacaacagcaacaaaaccttcaaaatttacaagtctttaagaaatagaa \textbf{ATGgca}\\toggcttcgcgtgggtggaggaggcgcggctgcag$ gtctttaagaaatagaa \textbf{ATGgca}	195
1		M A	2
196 16		tccaaaagagctctggtcatcctagccaaaggagcagaggagatggagacagtgattcctgtgga S K R A L V I L A K G A E E M E T V I P V D	
261 38		catcatgcggcgagctgggattaaagtcaccgttgcaggcttggctgggaaggaccccgtgcagt I M R R A G I K <u>V T V A G L A G K D P V Q</u> Peptide 1	
326 59		gtagccgtgatgtagtgatttgtccggataccagtctggaagaagcaaaacacagggaccatac CSRDVVICPDTSLEEAKTQGPY	390 67
391 81		gatgtggttgttcttccaggaggaaatctgggtgcacagaacttatctgagtcggctttggtgaa D V V V L P G G N L G A Q N L S E S A L V K	
456 103		ggagatcctcaaggagcaggagaacaggaagggcctcatagctgccatctgtgcgggtcctacgg <u>E I L K</u> E Q E N R K G L I A A I C A G P T Peptide 2 *	520 110
521 124		ccctgctggctcacgaagtaggctttggatgcaaggttacatcgcacccattggctaaggacaaa A L L A H E V G F G C K V <u>T S H P L A K</u> D K Peptide 3	585 132
586 146		atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggcctcatcctcac M M N G S H Y S Y S E S R V E K <u>D G L I L T</u> Peptide 4	
651 168		cagccgtgggcctgggaccagcttcgagtttgcgctggccattgtggaggcactcagtggcaagg SRGPGTSFEFALAIVEALSGK	715 175
716 189		acatggctaaccaagtgaaggccccgcttgttctcaaagacTAGagagcccaagccctggaccct D M A N Q V K A P L V L K D *	780 189
781		ggacccccaggctgagcaggcattggaagcccactagtgtgtccacagcccagtgaacctggcat	845
846	5	tggaagcccactagtgtgtccacagcccagtgaacctcaggaactaacgtgtgaagtagcccgct	910
911	-	gctcaggaatctcgccctggctctgtactattctgagccttgctagtagaataaacagttcccca	975
976	5	agetc*c*tgacggct*	985

Figure 3

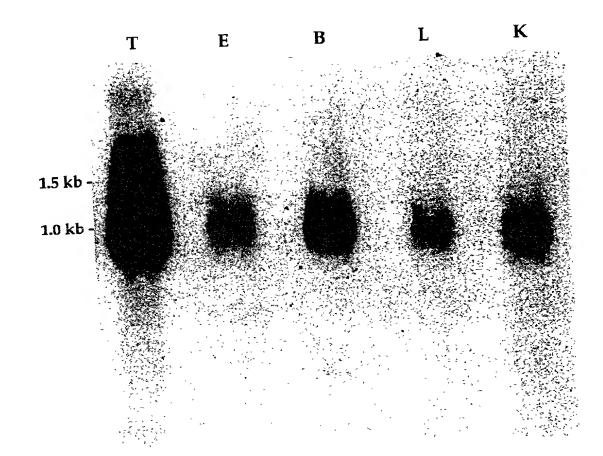


Figure 4

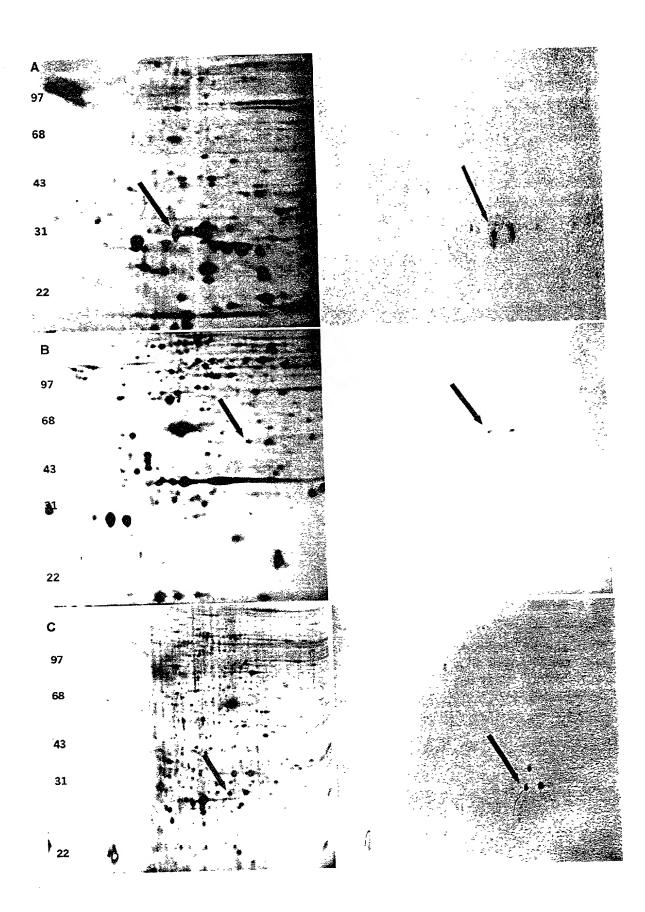
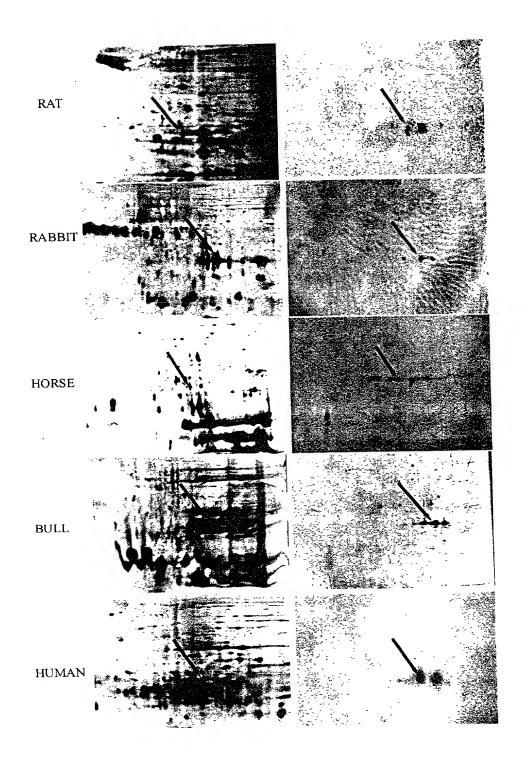
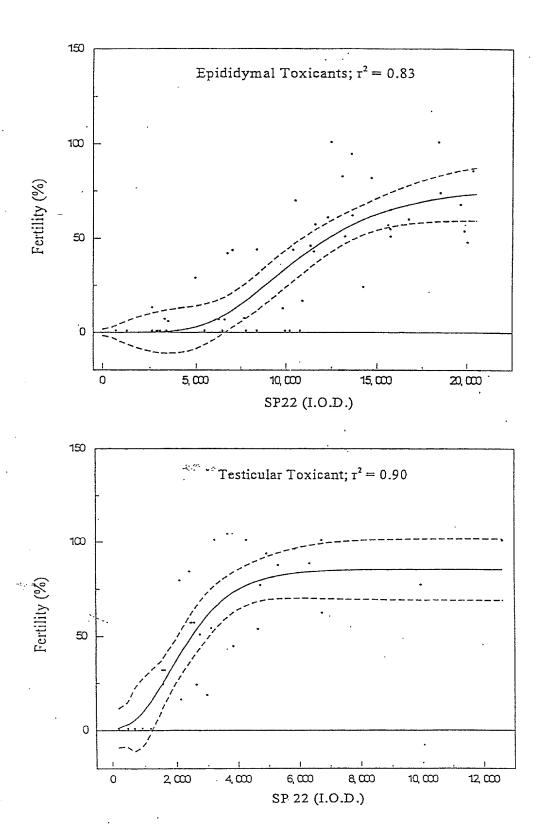
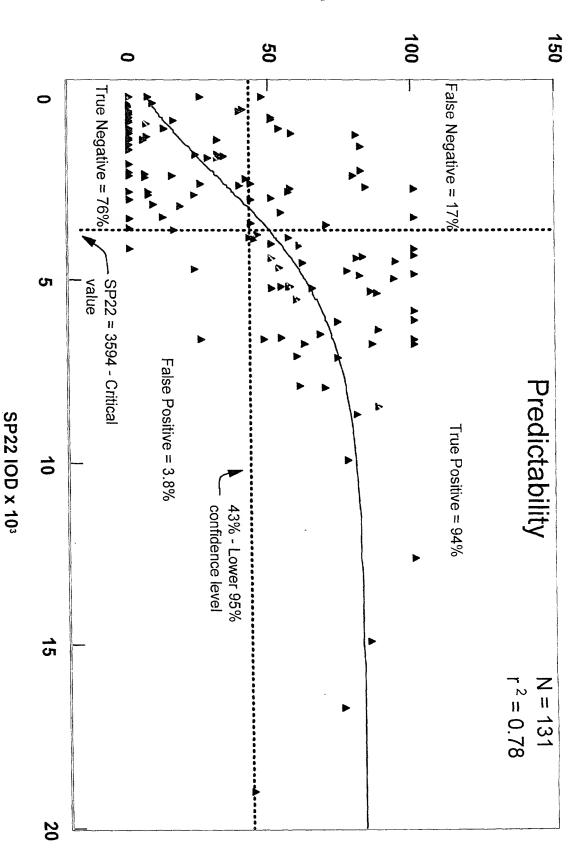


Figure 5





Fertility %



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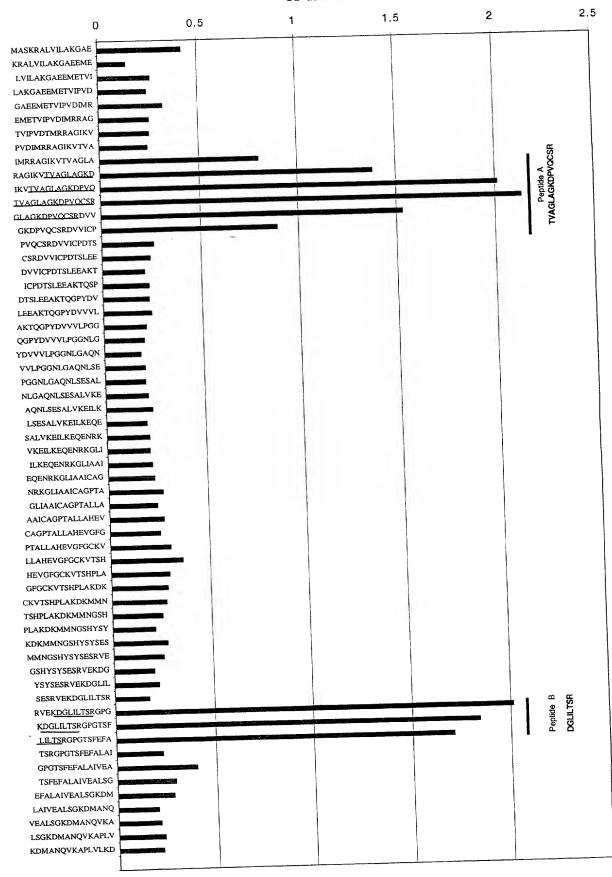


Figure 9

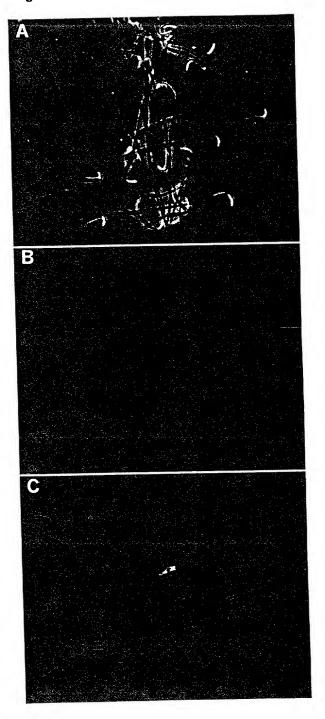
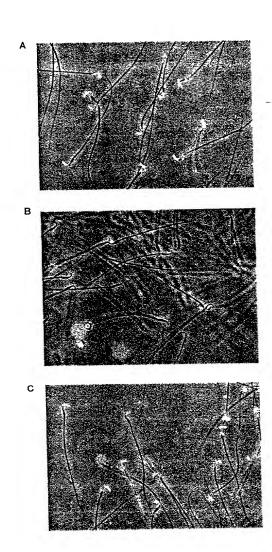
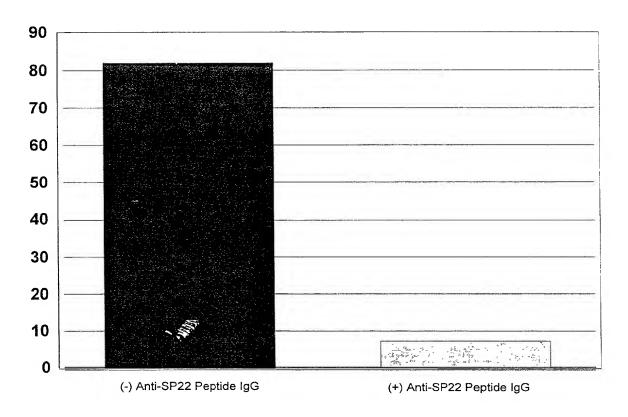
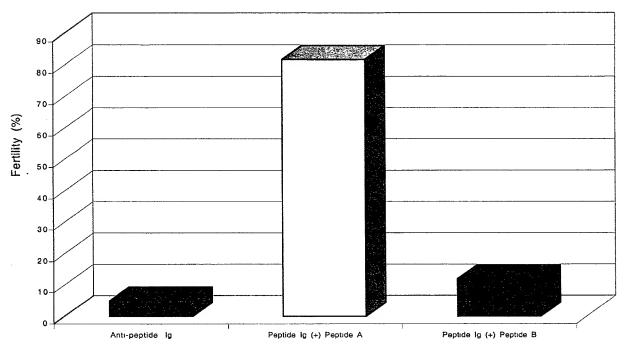


Figure 10









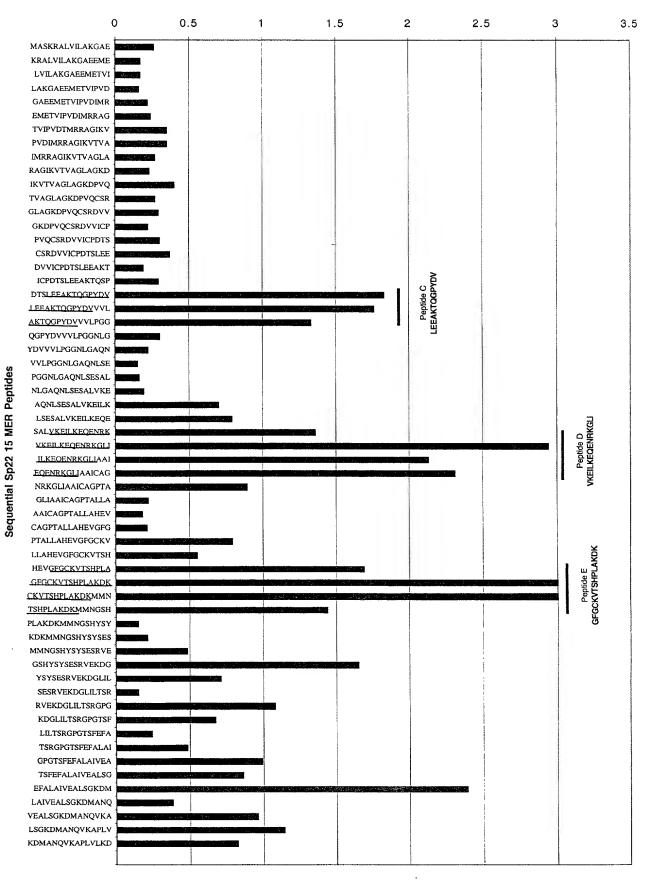
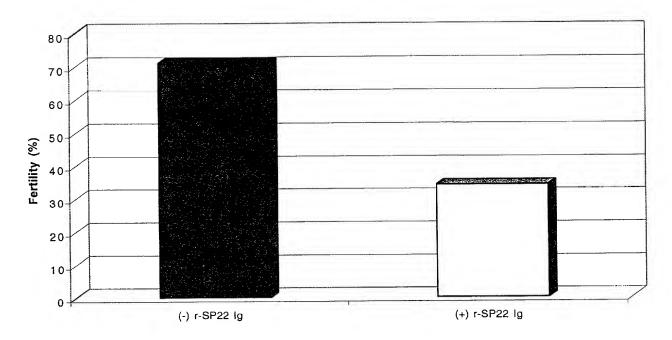
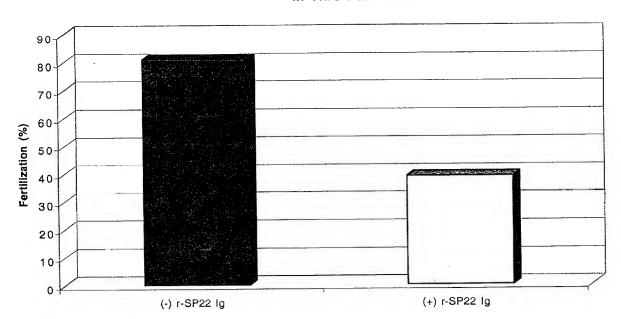


Figure 14

In Utero Insemination



In Vitro Fertilization



F1G. 15.

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33	aaa	gtc	acc	gtt	gca	ggc	ttg	gct	aaa	aag	gac	ccc	gtg	cag	gtgi	tag	ccg	tgai	tgt	agt	gat	tt	gt	198
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397	aa	atg	caa	ggt	tac	atc	gca	ccc	att	ggc	taa	.gga	caa	aat	gat	ga	acg	gcaç	jtc	act	aca	gct	tac	462
133	G	C	K	v	Т	s	H	P	L	A	K	D	ř	7	1 1	4 :	N (G \$	3 1	H '	Y	S	Y	154
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59	5 gi	ttct	cca	aaga	acta	agag	gago	cce	aago	ccct	tgg.	acc	ctg	gac	ccc	caç	ggct	gag	caç	igca	att	gga	ago	660
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66	1 c	cac	tag	aga	gac	cac	agc	cca	gtg	aac	ctg	gca	ttg	gaa	gco	cca	cta	gtgt	gto	ca	cag	cc	cag	t 726
72	7 g	aac	ctc	agg	aac	taa	cgt	gtg	aag	tag	ccc	gct	gct	caç	ggaa	atc	tcg	ccct	:99	etc	tgt	ac	tat	t 792
75	3 c	tga	gcc	ttg	cta	gta	gaa	taa	aca	gtt	ccc	caa	gct	c										83(

SP22(A)

FIGURE 16

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6	tagtgtggtcagagacttagcaccattggtctcccccaacctggtccagacatttcagcagttta 1	.30
131	- toggaacagcaacaacaacaaacottcaaaatttacaagtotttaagaaatagaaATGgca 1 M. A. 2	
196	tccaaaagagctct.ggtcatcctagccaaaggagcagagagagatggagacagtgattcctgtgga 2 S K R A I, V I L A K G A E E M E T V I P V D 2	
261 25	calcatgoggoga; ctgggattaaagtoacogttgcaggottggctgggaaggaccoogtgcagt 3	325 45
326 46	gtagecgtgatgtilgtgatttgtccggataccagtctggaagaagcaaaaacacagggaccatac : C S R D V V I C P D T S L E E A K T Q G P Y	390 67
391 68	gatgtggttgttcttccaggaggaaatctgggtgcacagaacttatctgagtcggctttggtgaa DVVVLPGGNLGAQNLSESALVK	
456 90	ggagatecteaaggageaggagaaeaggaagggeeteatagetgeeatetgtgegggteetaegg E I L K E Q E N R K G L I A A I C A G P T	520 110
521 111	ccctgctggctcacgaagtaggctttggatgcaaggttacatcgcacccattggctaaggacaaa A L L A + E V G F G C K V T S H P L A K D K	585 132
586 133	atgatgaacggcagtcactacagctactcagagagccgtgtggagaaggacggcctcatcctcac M M N G S H Y S Y S E S R V E K D G L I L T	
651 155	cageegtgggcci:gggaccagettegagtttgegetggecattgtggaggeactcagtggcaagg SRGPGTSFEFALAIVEALSCK	715 175
716 176	acatggctaacc.lagtgaaggccccgcttgttctcaaagacTAGagagcccaagccctggaccct D M A N ·2 V K A P L V L K D	780 189
781	ggacccccaggctgagcaggcattggaagcccactagtgtgtccacagcccagtgaacctggcat	845
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911	gctcaggaatctcgccctggctctgtactattctgagccttgctagtagaataaacagttcccca	. 97